RNA-seq profiling of pathogens in prosthetic joint infection

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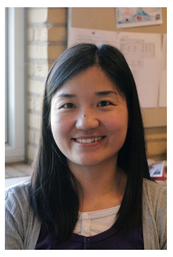

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Introduction

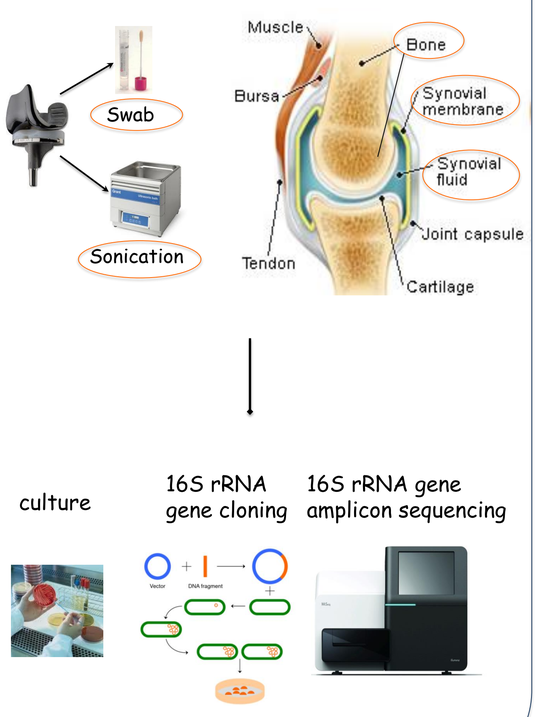
Prosthetic joint infections (PJIs) are serious complications of joint alloplasties. These device-associated infections are typically caused by bacteria growing in biofilms, which protect them from antimicrobial agents and host immune responses in poorly vascularized joints. Our current knowledge of how pathogens cope with the complex conditions within the host is based on *in vitro* studies and animal models, which can differ substantially from their behavior in the human host. Studying gene expression of pathogens during infection is a way to understand pathogenesis. RNA sequencing (RNA-seq) is capable of characterizing the entire transcriptome, both quantitatively and qualitatively, of an organism.

Aim

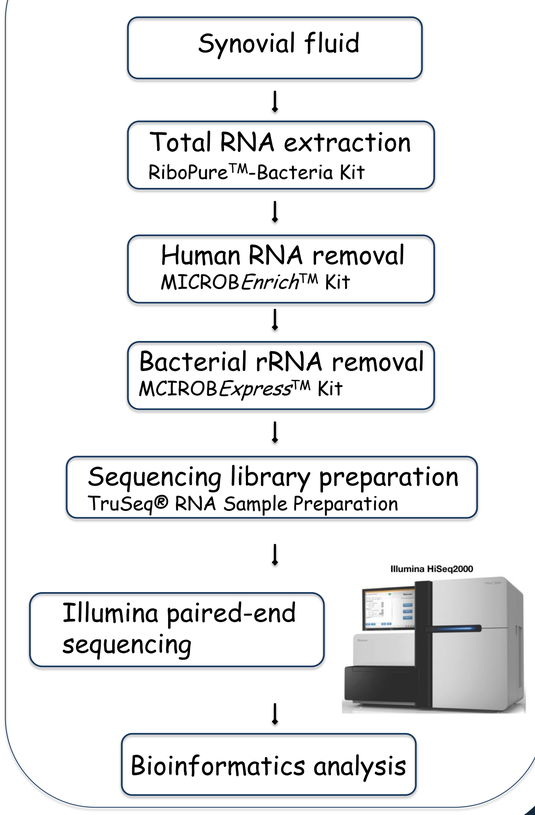
To study the gene expression of pathogens directly in PJI in a human host using RNA-seq.

Methods

Identification



RNA-seq



Conclusions

This study indicates that RNA-seq is a challenging but powerful tool to profile the gene expression of pathogens *in vivo*.

Results

Identification

Monomicrobial infection: *Staphylococcus aureus* was identified by 3 independent methods (culture, 16S rRNA gene cloning, and 16S rRNA gene amplicon sequencing).

Mapping statistics

	Number of reads	Number of paired reads
Total reads	23.000.000	11.500.000
S. aureus reads[1]	270.000 (1.17%)	113.000 (0.98%)
S. aureus mRNA reads	17.000 (0.074%)	7.000 (0.061%)

[1]Reference genome: *S. aureus* N315, 2.84 Mb, 2694 genes, 2613 proteins

Top 100 genes (ordered by RPKM)

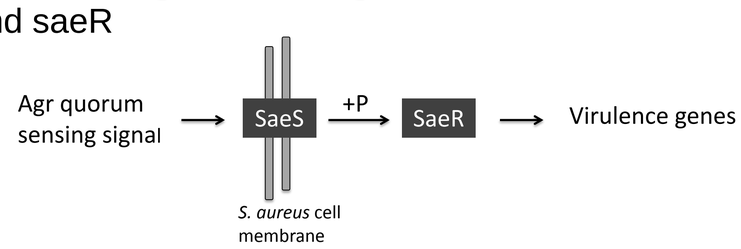
- 52 Essential genes
- 22 Hypothetical proteins
- 8 Infection related genes

Virulence factors:

- **hlgA**, **hlgB** and **hlgC** : form pores in immune cells
- **Sbi**: interferes with the host complement system

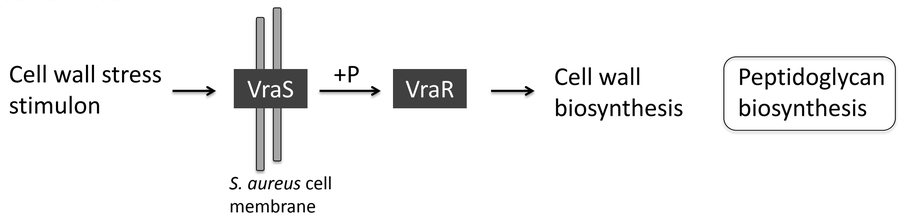
Virulence regulation genes:

saeS and saeR



Vancomycin resistance sensor/regulator:

vraS and vraR



Acknowledgement

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www.joint-prosthesis-infection-pain.dk